

Mail to  
Applicant

Page 1 of 1  
#9/FR  
10-03-01

1656

003  
RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001  
TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

4 <110> APPLICANT: Schweighoffer, Fabien  
5 Bracco, Laurent  
6 Tocque, Bruno  
8 <120> TITLE OF INVENTION: Qualitative Differential Screening  
11 <130> FILE REFERENCE: 50146/004002  
13 <140> CURRENT APPLICATION NUMBER: 09/623,828  
14 <141> CURRENT FILING DATE: 2000-11-30  
16 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00547  
17 <151> PRIOR FILING DATE: 1999-03-11  
19 <160> NUMBER OF SEQ ID NOS: 16  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 23  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Artificial Sequence  
28 <220> FEATURE:  
29 <223> OTHER INFORMATION: (Oligo)  
31 <221> NAME/KEY: misc\_feature  
32 <222> LOCATION: 13-19, 23  
33 <223> OTHER INFORMATION: n = A,T,C or G  
35 <400> SEQUENCE: 1  
W--> 36 gagaagcggtt atnnnnnnna ggn 23  
38 <210> SEQ ID NO: 2  
39 <211> LENGTH: 24  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: (Oligo)  
46 <221> NAME/KEY: misc\_feature  
47 <222> LOCATION: 13-20  
48 <223> OTHER INFORMATION: n = A,T,C or G  
50 <400> SEQUENCE: 2  
W--> 51 gagaagcggtt atnnnnnnnn tccc 24  
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54 <211> LENGTH: 23  
55 <212> TYPE: DNA  
56 <213> ORGANISM: Artificial Sequence  
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59 <223> OTHER INFORMATION: (Oligo)  
61 <221> NAME/KEY: misc\_feature  
62 <222> LOCATION: (13)...(23)  
63 <223> OTHER INFORMATION: n = A,T,C or G  
65 <400> SEQUENCE: 3  
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68 <210> SEQ ID NO: 4  
69 <211> LENGTH: 20  
70 <212> TYPE: DNA

Does Not Comply  
Corrected Diskette Needed

Not a valid <223> response.  
What is the source of the  
genetic material making up  
the artificial sequences?

See #11 on the Error  
Summary Sheet.

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Input Set : A:\50146.004002.SEQLIST.TXT  
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71 <213> ORGANISM: Artificial Sequence  
 73 <220> FEATURE:  
 74 <223> OTHER INFORMATION: *Oligo*  
 76 <221> NAME/KEY: misc\_feature  
 77 <222> LOCATION: (13)...(17)  
 78 <223> OTHER INFORMATION: n = A, T, C or G  
 80 <400> SEQUENCE: 4  
 W--> 81 **gagaagcgtt atnnnnncca** 20  
 83 <210> SEQ ID NO: 5  
 84 <211> LENGTH: 66  
 85 <212> TYPE: DNA  
 86 <213> ORGANISM: Homo sapiens  
 88 <400> SEQUENCE: 5  
 89 ccacacctgg ccagtatgtg ctcactggct tgcagagtgg gcagccagcc taagcatttg 60  
 90 cactgg 66  
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 93 <211> LENGTH: 23  
 94 <212> TYPE: DNA  
 95 <213> ORGANISM: Artificial Sequence  
 97 <220> FEATURE:  
 98 <223> OTHER INFORMATION: *Oligo*  
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 103 <210> SEQ ID NO: 7  
 104 <211> LENGTH: 22  
 105 <212> TYPE: DNA  
 106 <213> ORGANISM: Artificial Sequence  
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 109 <223> OTHER INFORMATION: *Oligo*  
 111 <400> SEQUENCE: 7  
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 114 <210> SEQ ID NO: 8  
 115 <211> LENGTH: 96  
 116 <212> TYPE: DNA  
 117 <213> ORGANISM: Homo sapiens  
 119 <400> SEQUENCE: 8  
 120 gtacgggaga gcacgaccac acctggccag tatgtgctca ctggcttgca gagtggcag 60  
 121 cctaaggatt tgctactggt ggaccctgag ggtgtg 96  
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 124 <211> LENGTH: 441  
 125 <212> TYPE: PRT  
 126 <213> ORGANISM: Homo sapiens  
 128 <400> SEQUENCE: 9  
 129 Met Asn Lys Leu Ser Gly Gly Gly Arg Arg Thr Arg Val Glu Gly  
 130 1 5 10 15  
 131 Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn  
 132 20 25 30  
 133 Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro  
 134 35 40 45

*See p. 1*

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Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

135 Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln  
136 50 55 60  
137 Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu  
138 65 70 75 80  
139 Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr  
140 85 90 95  
141 Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg  
142 100 105 110  
143 Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr  
144 115 120 125  
145 Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn  
146 130 135 140  
147 His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr  
148 145 150 155 160  
149 Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala  
150 165 170 175  
151 Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser  
152 180 185 190  
153 Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn  
154 195 200 205  
155 Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly  
156 210 215 220  
157 Ser Ala Trp Asp Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr  
158 225 230 235 240  
159 Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met  
160 245 250 255  
161 Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro  
162 260 265 270  
163 Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln  
164 275 280 285  
165 Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro  
166 290 295 300  
167 Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val  
168 305 310 315 320  
169 Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro  
170 325 330 335  
171 Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys  
172 340 345 350  
173 Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Gln Ser Val Ser  
174 355 360 365  
175 Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser  
176 370 375 380  
177 Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val  
178 385 390 395 400  
179 Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr  
180 405 410 415  
181 His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys  
182 420 425 430  
183 Leu Gln Gln Pro Val Glu Arg Lys Leu

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PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001  
TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

184 435 440  
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 188 <211> LENGTH: 1326  
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 190 <213> ORGANISM: Homo sapiens  
 192 <400> SEQUENCE: 10  
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 194 ggcgaggagt ggaccgcga cgggagcttt gtcaataagc ccacgcggg ctggctgcat 120  
 195 cccaacgaca aagtcatggg accccgggggtt tcctacttgg ttcggatcat gggttgtgt 180  
 196 gaggtcctcc agtcaatgcg tgccctggac ttcaacaccc ggactcaggt caccaggag 240  
 197 gccatcagtc tggtgtgtga ggctgtgcgg ggtgctaagg gggcgacaag gaggagaaag 300  
 198 cccctgttagcc gcccgcctag ctctatcctg gggaggagta acctgaaatt tgcttggatg 360  
 199 ccaatcactc tcaccgtctc caccagcagc ctcaacctca tggccgcaga ctgcaaacag 420  
 200 atcatcgcca accaccacat gcaatctatc tcatttgcattt ccggcgggaa tccggacaca 480  
 201 gccgagttatg tcgccttatgt tgccaaagac cctgtgaatc agagagcctg ccacattctg 540  
 202 gagtgtcccg aagggttgc ccaggatgtc atcagcacca ttggccagc cttcgagttg 600  
 203 cgcttcaaac aatacctcgaa accccaccc aaactgttca cccctcatga caggatggct 660  
 204 ggctttgatg gtcagcatg ggatgaggag gaggaagagc cacctgacca tcagttactat 720  
 205 aatgacttcc cggggaaagg acccccccctt ggggggggtgg tagacatgag gttcgggaa 780  
 206 ggagccgctc caggggctgc tcgaccact gcaccatgc cccagacccc cagccacttg 840  
 207 ggagctacat tgcctgttagg acagcctgtt gggggagatc cagaagtccg caaacagatg 900  
 208 ccaacctccac caccctgtcc aggccagagag ctttttgcattt atcccttcata tgtcaacgtg 960  
 209 cagaacctag acaaggcccc gcaaggcgtg ggtggtgctg gcccccccaa tcctgtatc 1020  
 210 aatggcgttgc caccgggaa cctgtttgac atgaaggccct tcgaagatgc ttttcgggtg 1080  
 211 cctccacccccc cccagtcgggt gtccatggct gagcagctcc gagggggagcc ctgggtccat 1140  
 212 gggaaagctga gcccggggaa ggctgaggca ctgctgcagc tcaatgggaa cttttgggtt 1200  
 213 cgactaagg atcaccgttt tgaaagtgtc agtcacccat tcaagctacca catggacaat 1260  
 214 cacttgcaca tcatctctgc gggcagcggaa ctgtgtctac agcaacctgt ggagcggaaa 1320  
 215 ctgtga 1326  
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 218 <211> LENGTH: 19  
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 220 <213> ORGANISM: Artificial Sequence  
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 223 <223> OTHER INFORMATION: Oligo  
 225 <400> SEQUENCE: 11  
 226 tgcccaaatac aacaagagc  
 228 <210> SEQ ID NO: 12  
 229 <211> LENGTH: 19  
 230 <212> TYPE: DNA  
 231 <213> ORGANISM: Artificial Sequence  
 233 <220> FEATURE:  
 234 <223> OTHER INFORMATION: Oligo  
 236 <400> SEQUENCE: 12  
 237 cccctgacaa gcctgaata 19  
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 240 <211> LENGTH: 24  
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 242 <213> ORGANISM: Artificial Sequence

See p.1

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/623,828

DATE: 06/14/2001  
TIME: 10:12:06

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

244 <220> FEATURE:  
245 <223> OTHER INFORMATION: Oligo 24  
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248 atgtctcaga gcaaccggga gctg  
250 <210> SEQ ID NO: 14  
251 <211> LENGTH: 24  
252 <212> TYPE: DNA  
253 <213> ORGANISM: Artificial Sequence  
255 <220> FEATURE:  
256 <223> OTHER INFORMATION: Oligo 24  
258 <400> SEQUENCE: 14  
259 gtggctccat tcaccgcggg gctg  
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262 <211> LENGTH: 19  
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264 <213> ORGANISM: Artificial Sequence  
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270 tgccaagaag ggaaggagt  
272 <210> SEQ ID NO: 16  
273 <211> LENGTH: 20  
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275 <213> ORGANISM: Artificial Sequence  
277 <220> FEATURE:  
278 <223> OTHER INFORMATION: Oligo 20  
280 <400> SEQUENCE: 16  
281 tgtcatgact ccagcaatag

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/623,828

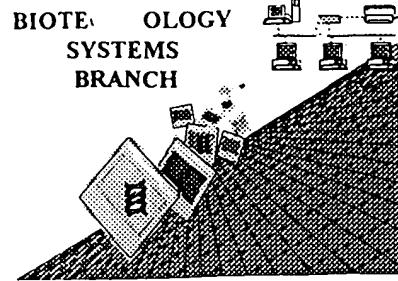
DATE: 06/14/2001

TIME: 10:12:07

Input Set : A:\50146.004002.SEQLIST.TXT  
Output Set: N:\CRF3\06142001\I623828.raw

L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/623, 828  
Source: 1656  
Date Processed by STIC: 6-14-01

RECEIVED  
JUL 09 2001  
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/623, 828

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)                   . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." (Please explain source of genetic material in <220> to <223> section.)  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.